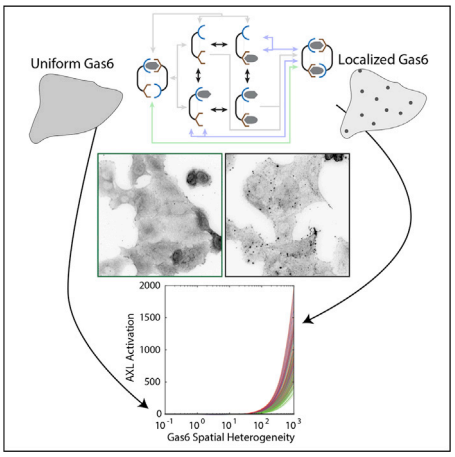
Cell Systems

In This Issue

CellPress



Sensing Cell Debris

MEYER ET AL., PAGE 25

Understanding the relationship between two ligand-binding sites on the AXL receptor explains how it senses localized concentrations of ligand.

Editor's note: The introduction of a "spatial inhomogeneity" parameter into the authors' mathematical model is the key to unlocking the molecular mechanisms at work in stimulating AXL signaling. See also Preview by Whitty.

Advancing Healthcare with Apps

MANDL ET AL., PAGE 8

Recent initiatives spurring the standardization of application programming interfaces to access electronic health records will support an ecosystem of apps that foster innovation in healthcare.

Editor's note: Many major electronic health record vendors are implementing APIs to allow third-party access to data, bringing the authors' vision closer to fruition (http://smarthealthit.org/).

Positive Gradients

Q&A, PAGE 2

The new vice chancellor of computational heath sciences at the University of California San Diego reflects on the coming era of big data in medicine.

Unraveling Redundancy

LEE ET AL., PAGE 37

Automated image analysis of unperturbed cells places the formin mDia1 at the top of the chain of molecular events driving cell protrusion.

Editor's note: This work describes both a general approach for analyzing the data from imaging fluctuations, pioneered by the Danuser lab, and places a new molecular player ahead of Arp2/3, which for almost two decades has been described as a master regulator of actin assembly. See also Preview by Gupton and Barzik.

Personal Regulomes

QU ET AL., PAGE 51

Genome-wide profiling of chromatin accessibility from standard clinical blood draws reveals regulatory variation between human individuals.

Editor's note: The use of multiple samples per individual and bioinformatics analysis were essential to identifying elements that reproducibly vary across individuals but not between replicate samples from the same individual. This work sets the stage for the application of chromatin-accessibility profiling to primary tissues and clinical samples. See also Preview by Maurano and Stamatoyannopoulos.

Engineering Gut Microbes

MIMEE ET AL., PAGE 62

A new collection of genetic parts for a microbe naturally abundant in the human gut provides tools for targeted manipulation of the microbiome.

Editor's note: The authors are the first to tailor a variety of tools to engineer a commensal microbe found in the human gut microbiome. Notably, the paper includes data showing the functioning of synthetic circuits in engineered microbes in vivo in the mouse gut. See also Preview by Donia.

Accelerated Yeast Editing

HORWITZ ET AL., PAGE 88

Improved delivery of Cas9 guide RNAs facilitates the addition of complete metabolic pathways and combinatorial testing of mutations in the yeast genome.

Editor's note: CRISPR-Cas9 has been used in yeast to knock out genes and introduce foreign DNA. Notable here is the multiplex knockin of combinations of alleles and genes.

Subway Sequencing

AFSHINNEKOO ET AL., PAGE 6

Analysis of DNA collected from all New York City subway stations provides a global view of an urban microbiome.

Editor's note: The data provide a resource for studying microbial diversity across a large built environment.